Pending Claims:

Claims 1-9 (Canceled)

Claim 10. (Previously Presented): A method for identifying a polypeptide that binds to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a mixture of polypeptides under conditions enabling binding between the support and a polypeptide of the mixture;

(c) washing the support to remove unbound polypeptides of the mixture; and

(d) identifying the polypeptide that binds to the support;

wherein a polypeptide that binds to the support is the polypeptide that binds to the peptide in the chosen protein.

Claim 11. (Previously Presented): The method of claim 10, wherein the polypeptide that binds to the peptide in the chosen protein binds to a high affinity domain of the chosen protein.

Claim 12. (Previously Presented): The method of claim 10, wherein the support is selected from the group consisting of a chip, bead, and plate.

Claim 13. (Previously Presented): The method of claim 10, wherein the set of support-attached overlapping peptides is synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 14. (Previously Presented): The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

Claim 15. (Previously Presented): The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

Claim 16. (Previously Presented): The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

Claim 17. (Previously Presented): The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

Claim 18. (Previously Presented): The method of claim 10, wherein the set of overlapping peptides is covalently attached to the support.

Claim 19. (Previously Presented): The method of claim 10, wherein the support is contacted with a lysate from a cell, wherein the lysate comprises the mixture of polypeptides.

Claim 20. (Previously Presented): The method of claim 10, wherein the chosen protein is human P-glycoprotein 1.

Claim 21. (Previously Presented): The method of claim 20, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

Claim 22. (Previously Presented): The method of claim 20, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO: 7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

Claim 23. (Previously Presented): The method of claim 20, wherein the polypeptide is tubulin.

Claim 24. (Previously Presented): The method of claim 10, wherein the chosen protein is human P-glycoprotein 3.

Claim 25. (Previously Presented): The method of claim 24, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

Claim 26. (Previously Presented): A method for identifying a peptide in a chosen protein that binds to a polypeptide, wherein said polypeptide is not an antibody, the method comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a polypeptide under conditions enabling binding between the support and the polypeptide;

(c) washing the support to remove unbound polypeptide; and

(d) identifying the peptide of the support that binds to the polypeptide.

Claim 27. (Previously Presented): The method of claim 26, wherein the peptide of the support that binds to the polypeptide is included within a high affinity domain of the chosen protein.

Claim 28. (Previously Presented): The method of claim 26, wherein the support is contacted with the mixture of polypeptides under conditions enabling binding between the support and the polypeptide of the mixture.

Claim 29. (Previously Presented): The method of claim 26, wherein the support is selected from the group consisting of a chip, bead, and plate.

Claim 30. (Previously Presented): The method of claim 26, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 31. (Previously Presented): The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

Claim 32. (Previously Presented): The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

Claim 33. (Previously Presented): The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

Claim 34. (Previously Presented): The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

Claim 35. (Previously Presented): The method of claim 26, wherein the set of overlapping peptides is covalently attached to the support.

Claim 36. (Previously Presented): The method of claim 26, wherein the chosen protein is human P-glycoprotein 1.

Claim 37. (Previously Presented): The method of claim 36, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

Claim 38. (Previously Presented): The method of claim 36, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO:7 and a second peptide consisting of an amino acid sequence of SEQ ID NO:8.

Claim 39. (Previously Presented): The method of claim 36, wherein the polypeptide is tubulin.

Claim 40. (Previously Presented): The method of claim 26, wherein the chosen protein is human P-glycoprotein 3.

Claim 41. (Previously Presented): The method of claim 40, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

Claim 42. (Previously Presented): A method of identifying a compound that modulates the binding of a polypeptide to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a candidate compound and the polypeptide under conditions enabling binding between the support and the polypeptide;

(c) washing the support to remove unbound polypeptides of the mixture; and

(d) detecting binding of the polypeptide to the support;

wherein a change in the binding of the polypeptide to the support in the presence of the candidate compound compared to the binding of the polypeptide to the support in the absence of

the candidate compound identifies the candidate compound as a compound that modulates binding of the polypeptide to the peptide in the chosen protein.

Claim 43. (Previously Presented): The method of claim 42, wherein the domain of the chosen protein is a high affinity domain of the chosen protein.

Claim 44. (Previously Presented): The method of claim 42, wherein the polypeptide is known to bind to the chosen protein.

Claim 45. (Previously Presented): The method of claim 42, wherein the support is selected from the group consisting of a chip, bead, and plate.

Claim 46. (Previously Presented): The method of claim 42, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 47. (Previously Presented): The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

Claim 48. (Previously Presented): The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

Claim 49. (Previously Presented): The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

Claim 50. (Previously Presented): The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

Claim 51. (Previously Presented): The method of claim 42, wherein the set of overlapping peptides is covalently attached to the support.

Claim 52. (Previously Presented): The method of claim 42, wherein the chosen protein is human P-glycoprotein 1.

Claim 53. (Previously Presented): The method of claim 52, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3 and a combination of the first, second, and third domains.

Claim 54. (Previously Presented): The method of claim 52, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO: 7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

Claim 55. (Previously Presented): The method of claim 52, wherein the polypeptide is tubulin.

Claim 56. (Previously Presented): The method of claim 42, wherein the chosen protein is human P-glycoprotein 3.

Claim 57. (Previously Presented): The method of claim 56, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

Claim 58. (Previously Presented): A support to which is attached a set of overlapping peptides spanning a complete sequence of at least a domain of a protein.

Claim 59. (Previously Presented): The support of claim 58, wherein the domain of the protein is a high affinity domain of the protein.

Claim 60. (Previously Presented): The support of claim 58, wherein set of overlapping peptides spans the complete sequence of the entire protein.

Claim 61. (Previously Presented): The support of claim 58, wherein the support is selected from the group consisting of a chip, bead, and plate.

Claim 62. (Previously Presented): The support of claim 58, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 63. (Previously Presented): The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

Claim 64. (Previously Presented): The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

Claim 65. (Previously Presented): The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

Claim 66. (Previously Presented): The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

Claim 67. (Previously Presented): The support of claim 58, wherein the set of overlapping peptides is covalently attached to the support.

Claim 68. (Previously Presented): The support of claim 58, wherein a polypeptide that binds to a peptide attached to the support is identified as a polypeptide that binds to the protein.

Claim 69. (Previously Presented): The support of claim 58, wherein the chosen protein is human P-glycoprotein 1.

Claim 70. (Previously Presented): The support of claim 69, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID

NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

Claim 71. (Previously Presented): The support of claim 69, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO:7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

Claim 72. (Previously Presented): The support of claim 58, wherein the chosen protein is human P-glycoprotein 3.

Claim 73. (Previously Presented): The support of claim 72, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

Claim 74. (Previously Presented): A method for purifying tubulin comprising:

a) contacting a sample containing tubulin with a support to which is attached a first peptide consisting of an amino acid sequence of RSSLIR and a second peptide consisting of an amino acid sequence of SVRGSQ, wherein the contacting is under conditions enabling binding between the support and the tubulin in the same;

b) rinsing the sample-contacted support to remove unbound molecules in said sample; and

c) eluting said tubulin bound to said support;

wherein said tubulin eluted from said support is purified.